

SEQUENCE LISTING

<110> Jegla, Timothy James  
ICAGen, Inc.

<120> Kv10.1, a Novel Voltage-Gated Potassium Channel From  
Human Brain

<130> 018512-005910US

<140> US 09/833,466  
<141> 2001-04-11

<150> US 60/197,793  
<151> 2000-04-14

<160> 18

<170> PatentIn Ver. 2.1

<210> 1  
<211> 2103  
<212> DNA  
<213> Homo sapiens

<220>  
<223> human alpha subunit of voltage-gated potassium  
channel Kv10.1

<220>  
<221> CDS  
<222> (151)..(1788)  
<223> Kv10.1

<400> 1  
ggcaatgtct gagcccctag ctgtgctggc ccgggctggc ctctctaaga cagtgcaggc 60  
cacgtgatcc atccctcttag aggcagttag caggtgaggg acccctacca cagccaggag 120  
aaaaaaacta ggcgtccact ttccgcagcc atgctcaaac agagttagag gagacggtcc 180  
tggagctaca ggccttgaa cacgacggag aatgagggca gccaaacaccg caggagcatt 240  
tgctccctgg gtgccccgttc cggctcccag gccagcatcc acggctggac agagggcaac 300  
tataactact acatcgagga agacgaagac ggggaggagg aggaccagtg gaaggacgac 360  
ctggcagaag aggaccagca ggcaggggag gtcaccaccc ccaagcccga gggcccccagc 420  
gaccctccgg ccctgctgtc cacgctaat gtgaacgtgg gtggccacag ctaccagctg 480  
gactactgcg agctggccgg ctcccccaag acgcgcctag gtcgcctggc cacccacc 540  
agccgcagcc gccagctaag cctgtgcgac gactacgagg agcagacaga cgaataactc 600  
ttcgaccgcg accggccgt cttccagctg gtctacaatt tctacctgtc cgggggtgtc 660  
ctgggtctcg acgggctgtg tccgcgcgc ttccctggagg agctgggcta ctggggcgtg 720  
cggtcaagt acacgcccacg ctgctgcgc atctgcttcg aggagcggcg cgacgagctg 780  
agcgaacggc tcaagatcca gcacgagctg cgccgcgcagg cgccaggctcgaa ggaggcggag 840  
gaactctcc gcacatgcg cttctacggc cccgacgcgc gccgcctctg gaaacctatg 900  
gagaagccat tctccctcggt ggccgccaag gccatcgggg tggcgtccag caccttcgtg 960  
ctcgctcccg tggtggcgct ggccgtcaac accgtggagg agatgcagca gcaactcgaaa 1020  
cagggcggagg gcggcccaaa cctgcggccc atccctggagc acgtggagat gctgtgcgt 1080  
ggcttctca cgctcgagta cctgctgcgc ctgcctcca cggccgcacct gaggcgcttc 1140  
gcgcgcagcg ccctcaaccc ggtggacctg gtggccatcc tgccgtctca ctttcagctg 1200  
ctgctcgagt gcttcacggg cgagggccac caacgcggcc agacgggtggg cagcgtgggt 1260  
aagggtggtc aggtgttgcg cgtcatgcgc ctcatgcga tcttccgcatt cctcaagctg 1320  
gcgcgcact ccacccggact gcgtgccttc ggcttcacgc tgccgcactg ctaccagcag 1380  
gtgggctgcc tgctgctctt catgcgcattt ggcatttca ctccctctgc ggctgtctac 1440  
tctgtggagc acgtatgtgcc cagcaccaac ttcaactacca tcccccaactc ctggtgggtgg 1500  
ggccgcgtga gcatctccac cgtggctac ggagacatgt acccagagac ccacccctggc 1560

aggtttttg ctttcctctg cattgctttt gggatcattc tcaacggat gcccattcc 1620  
 atcctctaca acaagtttc tgattactac agcaagctga aggcttatga gtataccacc 1680  
 atacgcagg agagggaga ggtgaacttc atgcagagag ccagaaaagaa gatagcttag 1740  
 tggcgctg gaagcaaccc acagctcacc ccaagacaag agaatttagta ttttatagga 1800  
 catgtggctg gtagattcca tgaactcaa ggcttcattt ctctttttt aatcattatg 1860  
 attggcagca aaaggaaatg tgaagcagac atacacaaag gccatttcgt tcacaaagta 1920  
 ctgcctctag aaatactcat tttggccaa actcagaatg tctcatagtt gctctgtgtt 1980  
 gtgtgaaaca tctgaccttc tcaatgacgt tgatattgaa aacctgaggg gagcaacagc 2040  
 ttagattttt cttgttagctt ctcgtggcat ctagctaata aatattttt ggacttgaaa 2100  
 aaa 2103

<210> 2  
 <211> 1638  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human alpha subunit of voltage-gated potassium  
 channel Kv10.1 coding sequence

<220>  
 <221> CDS  
 <222> (1)..(1638)  
 <223> Kv10.1

<400> 2

atg	ctc	aaa	cag	agt	gag	agg	aga	cgg	tcc	tgg	agc	tac	agg	ccc	tgg		48
Met	Leu	Lys	Gln	Ser	Glu	Arg	Arg	Arg	Ser	Trp	Ser	Tyr	Arg	Pro	Trp		
1																15	

aac acg acg gag aat gag ggc agc caa cac cgc agg agc att tgc tcc 96  
 Asn Thr Thr Glu Asn Glu Gly Ser Gln His Arg Arg Ser Ile Cys Ser  
 20 25 30

ctg ggt gcc cgt tcc ggc tcc cag gcc agc atc cac ggc tgg aca gag 144  
 Leu Gly Ala Arg Ser Gly Ser Gln Ala Ser Ile His Gly Trp Thr Glu  
 35 40 45

ggc aac tat aac tac tac atc gag gaa gac gaa gac ggg gag gag gag 192  
 Gly Asn Tyr Asn Tyr Tyr Ile Glu Glu Asp Glu Asp Gly Glu Glu Glu  
 50 55 60

gac cag tgg aag gac gac ctg gca gaa gag gac cag cag gca ggg gag 240  
 Asp Gln Trp Lys Asp Asp Leu Ala Glu Asp Gln Gln Ala Gly Glu  
 65 70 75 80

gtc acc acc gcc aag ccc gag ggc ccc agc gac cct ccg gcc ctg ctg 288  
 Val Thr Thr Ala Lys Pro Glu Gly Pro Ser Asp Pro Pro Ala Leu Leu  
 85 90 95

tcc acg ctg aat gtg aac gtg ggt ggc cac agc tac cag ctg gac tac 336  
 Ser Thr Leu Asn Val Asn Val Gly Gly His Ser Tyr Gln Leu Asp Tyr  
 100 105 110

tgc gag ctg gcc ggc ttc ccc aag acg cgc cta ggt cgc ctg gcc acc 384  
 Cys Glu Leu Ala Gly Phe Pro Lys Thr Arg Leu Gly Arg Leu Ala Thr  
 115 120 125

tcc acc agc cgc agc cgc cag cta agc ctg tgc gac gac tac gag gag	432
Ser Thr Ser Arg Ser Arg Gln Leu Ser Leu Cys Asp Asp Tyr Glu Glu	
130 135 140	
cag aca gac gaa tac ttc ttc gac cgc gac ccg gcc gtc ttc cag ctg	480
Gln Thr Asp Glu Tyr Phe Phe Asp Arg Asp Pro Ala Val Phe Gln Leu	
145 150 155 160	
gtc tac aat ttc tac ctg tcc ggg gtg ctg ctg gtg ctc gac ggg ctg	528
Val Tyr Asn Phe Tyr Leu Ser Gly Val Leu Leu Val Leu Asp Gly Leu	
165 170 175	
tgt ccg cgc cgc ttc ctg gag gag ctg ggc tac tgg ggc gtg cgg ctc	576
Cys Pro Arg Arg Phe Leu Glu Leu Gly Tyr Trp Gly Val Arg Leu	
180 185 190	
aag tac acg cca cgc tgc tgc cgc atc tgc ttc gag gag cgg cgc gac	624
Lys Tyr Thr Pro Arg Cys Cys Arg Ile Cys Phe Glu Glu Arg Arg Asp	
195 200 205	
gag ctg agc gaa cgg ctc aag atc cag cac gag ctg cgc gcg cag gcg	672
Glu Leu Ser Glu Arg Leu Lys Ile Gln His Glu Leu Arg Ala Gln Ala	
210 215 220	
cag gtc gag gag gcg gag gaa ctc ttc cgc gac atg cgc ttc tac ggc	720
Gln Val Glu Glu Ala Glu Glu Leu Phe Arg Asp Met Arg Phe Tyr Gly	
225 230 235 240	
ccg cag cgg cgc cgc ctc tgg aac ctc atg gag aag cca ttc tcc tcg	768
Pro Gln Arg Arg Arg Leu Trp Asn Leu Met Glu Lys Pro Phe Ser Ser	
245 250 255	
gtg gcc aag gcc atc ggg gtg gcg tcc agc acc ttc gtg ctc gtc	816
Val Ala Ala Lys Ala Ile Gly Val Ala Ser Ser Thr Phe Val Leu Val	
260 265 270	
tcc gtg gtg gcg ctg gcg ctc aac acc gtg gag gag atg cag cag cac	864
Ser Val Val Ala Leu Ala Leu Asn Thr Val Glu Glu Met Gln Gln His	
275 280 285	
tcg ggg cag ggc gag ggc cca gac ctg cgg ccc atc ctg gag cac	912
Ser Gly Gln Gly Glu Gly Gly Pro Asp Leu Arg Pro Ile Leu Glu His	
290 295 300	
gtg gag atg ctg tgc atg ggc ttc ttc acg ctc gag tac ctg ctg cgc	960
Val Glu Met Leu Cys Met Gly Phe Phe Thr Leu Glu Tyr Leu Leu Arg	
305 310 315 320	
cta gcc tcc acg ccc gac ctg agg cgc ttc gcg cgc agc gcc ctc aac	1008
Leu Ala Ser Thr Pro Asp Leu Arg Arg Phe Ala Arg Ser Ala Leu Asn	
325 330 335	
ctg gtg gac ctg gtg gcc atc ctg ccg ctc tac ctt cag ctg ctg ctc	1056
Leu Val Asp Leu Val Ala Ile Leu Pro Leu Tyr Leu Gln Leu Leu Leu	
340 345 350	
gag tgc ttc acg ggc gag ggc cac caa cgc ggc cag acg gtg ggc agc	1104
Glu Cys Phe Thr Gly Glu Gly His Gln Arg Gly Gln Thr Val Gly Ser	
355 360 365	

gtg ggt aag gtg ggt cag gtg ttg cgc gtc atg cgc ctc atg cgc atc Val Gly Lys Val Gly Gln Val Leu Arg Val Met Arg Leu Met Arg Ile 370	375	380	1152	
ttc cgc atc ctc aag ctg gcg cgc cac tcc acc gga ctg cgt gcc ttc Phe Arg Ile Leu Lys Leu Ala Arg His Ser Thr Gly Leu Arg Ala Phe 385	390	395	400	1200
ggc ttc acg ctg cgc cag tgc tac cag cag gtg ggc tgc ctg ctg ctc Gly Phe Thr Leu Arg Gln Cys Tyr Gln Gln Val Gly Cys Leu Leu 405	410	415	1248	
ttc atc gcc atg ggc atc ttc act ttc tct gcg gct gtc tac tct gtg Phe Ile Ala Met Gly Ile Phe Thr Phe Ser Ala Ala Val Tyr Ser Val 420	425	430	1296	
gag cac gat gtg ccc agc acc aac ttc act acc atc ccc cac tcc tgg Glu His Asp Val Pro Ser Thr Asn Phe Thr Thr Ile Pro His Ser Trp 435	440	445	1344	
tgg tgg gcc gcg gtg agc atc tcc acc gtg ggc tac gga gac atg tac Trp Trp Ala Ala Val Ser Ile Ser Thr Val Gly Tyr Gly Asp Met Tyr 450	455	460	1392	
cca gag acc cac ctg ggc agg ttt ttt gcc ttc ctc tgc att gct ttt Pro Glu Thr His Leu Gly Arg Phe Phe Ala Phe Leu Cys Ile Ala Phe 465	470	475	480	1440
ggg atc att ctc aac ggg atg ccc att tcc atc ctc tac aac aag ttt Gly Ile Ile Leu Asn Gly Met Pro Ile Ser Ile Leu Tyr Asn Lys Phe 485	490	495	1488	
tct gat tac tac agc aag ctg aag gct tat gag tat acc acc ata cgc Ser Asp Tyr Tyr Ser Lys Leu Lys Ala Tyr Glu Tyr Thr Thr Ile Arg 500	505	510	1536	
agg gag agg gga gag gtg aac ttc atg cag aga gca aga aag aag ata Arg Glu Arg Gly Glu Val Asn Phe Met Gln Arg Ala Arg Lys Lys Ile 515	520	525	1584	
gct gag tgt ttg ctt gga agc aac cca cag ctc acc cca aga caa gag Ala Glu Cys Leu Leu Gly Ser Asn Pro Gln Leu Thr Pro Arg Gln Glu 530	535	540	1632	
aat tag Asn 545			1638	

```

<210> 3
<211> 545
<212> PRT
<213> Homo sapiens
<223> human alpha subunit of voltage-gated potassium
channel Kv10.1

<220>
<221> PEPTIDE
<222> (102)..(514)
<223> conserved region of voltage-gated potassium
channel Kv10.1

```

<400> 3  
 Met Leu Lys Gln Ser Glu Arg Arg Arg Ser Trp Ser Tyr Arg Pro Trp  
     1               5                   10                   15  
 Asn Thr Thr Glu Asn Glu Gly Ser Gln His Arg Arg Ser Ile Cys Ser  
     20               25                   30  
 Leu Gly Ala Arg Ser Gly Ser Gln Ala Ser Ile His Gly Trp Thr Glu  
     35               40                   45  
 Gly Asn Tyr Asn Tyr Tyr Ile Glu Glu Asp Glu Asp Gly Glu Glu  
     50               55                   60  
 Asp Gln Trp Lys Asp Asp Leu Ala Glu Glu Asp Gln Gln Ala Gly Glu  
     65               70                   75                   80  
 Val Thr Thr Ala Lys Pro Glu Gly Pro Ser Asp Pro Pro Ala Leu Leu  
     85               90                   95  
 Ser Thr Leu Asn Val Asn Val Gly Gly His Ser Tyr Gln Leu Asp Tyr  
     100               105                   110  
 Cys Glu Leu Ala Gly Phe Pro Lys Thr Arg Leu Gly Arg Leu Ala Thr  
     115               120                   125  
 Ser Thr Ser Arg Ser Arg Gln Leu Ser Leu Cys Asp Asp Tyr Glu Glu  
     130               135                   140  
 Gln Thr Asp Glu Tyr Phe Phe Asp Arg Asp Pro Ala Val Phe Gln Leu  
     145               150                   155                   160  
 Val Tyr Asn Phe Tyr Leu Ser Gly Val Leu Leu Val Leu Asp Gly Leu  
     165               170                   175  
 Cys Pro Arg Arg Phe Leu Glu Leu Gly Tyr Trp Gly Val Arg Leu  
     180               185                   190  
 Lys Tyr Thr Pro Arg Cys Cys Arg Ile Cys Phe Glu Glu Arg Arg Asp  
     195               200                   205  
 Glu Leu Ser Glu Arg Leu Lys Ile Gln His Glu Leu Arg Ala Gln Ala  
     210               215                   220  
 Gln Val Glu Glu Ala Glu Glu Leu Phe Arg Asp Met Arg Phe Tyr Gly  
     225               230                   235                   240  
 Pro Gln Arg Arg Leu Trp Asn Leu Met Glu Lys Pro Phe Ser Ser  
     245               250                   255  
 Val Ala Ala Lys Ala Ile Gly Val Ala Ser Ser Thr Phe Val Leu Val  
     260               265                   270  
 Ser Val Val Ala Leu Ala Leu Asn Thr Val Glu Glu Met Gln Gln His  
     275               280                   285  
 Ser Gly Gln Gly Glu Gly Pro Asp Leu Arg Pro Ile Leu Glu His  
     290               295                   300  
 Val Glu Met Leu Cys Met Gly Phe Phe Thr Leu Glu Tyr Leu Leu Arg  
     305               310                   315                   320  
 Leu Ala Ser Thr Pro Asp Leu Arg Arg Phe Ala Arg Ser Ala Leu Asn  
     325               330                   335  
 Leu Val Asp Leu Val Ala Ile Leu Pro Leu Tyr Leu Gln Leu Leu Leu  
     340               345                   350  
 Glu Cys Phe Thr Gly Glu Gly His Gln Arg Gly Gln Thr Val Gly Ser  
     355               360                   365  
 Val Gly Lys Val Gly Gln Val Leu Arg Val Met Arg Leu Met Arg Ile  
     370               375                   380  
 Phe Arg Ile Leu Lys Leu Ala Arg His Ser Thr Gly Leu Arg Ala Phe  
     385               390                   395                   400  
 Gly Phe Thr Leu Arg Gln Cys Tyr Gln Gln Val Gly Cys Leu Leu Leu  
     405               410                   415  
 Phe Ile Ala Met Gly Ile Phe Thr Phe Ser Ala Ala Val Tyr Ser Val  
     420               425                   430  
 Glu His Asp Val Pro Ser Thr Asn Phe Thr Thr Ile Pro His Ser Trp  
     435               440                   445  
 Trp Trp Ala Ala Val Ser Ile Ser Thr Val Gly Tyr Gly Asp Met Tyr  
     450               455                   460  
 Pro Glu Thr His Leu Gly Arg Phe Phe Ala Phe Leu Cys Ile Ala Phe  
     465               470                   475                   480

Gly Ile Ile Leu Asn Gly Met Pro Ile Ser Ile Leu Tyr Asn Lys Phe  
485 490 495  
Ser Asp Tyr Tyr Ser Lys Leu Lys Ala Tyr Glu Tyr Thr Thr Ile Arg  
500 505 510  
Arg Glu Arg Gly Glu Val Asn Phe Met Gln Arg Ala Arg Lys Lys Ile  
515 520 525  
Ala Glu Cys Leu Leu Gly Ser Asn Pro Gln Leu Thr Pro Arg Gln Glu  
530 535 540  
Asn  
545

<210> 4  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:sense Oligo 1

<400> 4  
gccatgctca aacagagtga gaggagac

28

<210> 5  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:antisense Oligo  
2

<400> 5  
gagcgtgaag aagcccatgc acag

24

<210> 6  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:RACE PCR  
gene-specific antisense Oligo 3

<400> 6  
gcagcacccc ggacaggtag aaa

23

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:nested  
gene-specific antisense Oligo 4

<400> 7  
cggccgggtc gcggtcgaag aagt

24

```

<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:standard 3'
      RACE PCR nested Oligo 5

<400> 8
ccaccatag ggcagccaaac accgcaggag ca 32

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:new 3' RACE
      gene-specific sense Oligo 6

<400> 9
ggctgtctac tctgtggagc acgat 25

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense Oligo
      7

<400> 10
gagtatttct agagggcagta ctttgtg 27

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:coding region
      Oligo 8

<400> 11
attctcttgt ctgggggtga gctg 24

<210> 12
<211> 854
<212> PRT
<213> Homo sapiens

<220>
<223> human voltage-gated potassium channel Kv2.1

```

<400> 12

Met Thr Lys His Gly Ser Arg Ser Thr Ser Ser Leu Pro Pro Glu Pro  
1 5 10 15  
Met Glu Ile Val Arg Ser Lys Ala Cys Ser Arg Arg Val Arg Leu Asn  
20 25 30  
Val Gly Gly Leu Ala His Glu Val Leu Trp Arg Thr Leu Asp Arg Leu  
35 40 45  
Pro Arg Thr Arg Leu Gly Lys Leu Arg Asp Cys Asn Thr His Asp Ser  
50 55 60  
Leu Leu Glu Val Cys Asp Asp Tyr Ser Leu Asp Asp Asn Glu Tyr Phe  
65 70 75 80  
Phe Asp Arg His Pro Gly Ala Phe Thr Ser Ile Leu Asn Phe Tyr Arg  
85 90 95  
Thr Gly Arg Leu His Met Met Glu Glu Met Cys Ala Leu Ser Phe Ser  
100 105 110  
Gln Glu Leu Asp Tyr Trp Gly Ile Asp Glu Ile Tyr Leu Glu Ser Cys  
115 120 125  
Cys Gln Ala Arg Tyr His Gln Lys Lys Glu Gln Met Asn Glu Glu Leu  
130 135 140  
Lys Arg Glu Ala Glu Thr Leu Arg Glu Arg Glu Gly Glu Glu Phe Asp  
145 150 155 160  
Asn Thr Cys Cys Ala Glu Lys Arg Lys Lys Leu Trp Asp Leu Leu Glu  
165 170 175  
Lys Pro Asn Ser Ser Val Ala Ala Lys Ile Leu Ala Ile Ile Ser Ile  
180 185 190  
Met Phe Ile Val Leu Ser Thr Ile Ala Leu Ser Leu Asn Thr Leu Pro  
195 200 205  
Glu Leu Gln Ser Leu Asp Glu Phe Gly Gln Ser Thr Asp Asn Pro Gln  
210 215 220  
Leu Ala His Val Glu Ala Val Cys Ile Ala Trp Phe Thr Met Glu Tyr  
225 230 235 240  
Leu Leu Arg Phe Leu Ser Ser Pro Lys Lys Trp Lys Phe Phe Lys Gly  
245 250 255  
Pro Leu Asn Ala Ile Asp Leu Leu Ala Ile Leu Pro Tyr Tyr Val Thr  
260 265 270  
Ile Phe Leu Thr Glu Ser Asn Lys Ser Val Leu Gln Phe Gln Asn Val  
275 280 285  
Arg Arg Val Val Gln Ile Phe Arg Ile Met Arg Ile Leu Arg Ile Leu  
290 295 300  
Lys Leu Ala Arg His Ser Thr Gly Leu Gln Ser Leu Gly Phe Thr Leu  
305 310 315 320  
Arg Arg Ser Tyr Asn Glu Leu Gly Leu Leu Ile Leu Phe Leu Ala Met  
325 330 335  
Gly Ile Met Ile Phe Ser Ser Leu Val Phe Phe Ala Glu Lys Asp Glu  
340 345 350  
Asp Asp Thr Lys Phe Lys Ser Ile Pro Ala Ser Phe Trp Trp Ala Thr  
355 360 365  
Ile Thr Met Thr Thr Val Gly Tyr Gly Asp Ile Tyr Pro Lys Thr Leu  
370 375 380  
Leu Gly Lys Ile Val Gly Gly Leu Cys Cys Ile Ala Gly Val Leu Val  
385 390 395 400  
Ile Ala Leu Pro Ile Pro Ile Ile Val Asn Asn Phe Ser Glu Phe Tyr  
405 410 415  
Lys Glu Gln Lys Arg Gln Glu Lys Ala Ile Lys Arg Arg Glu Ala Leu  
420 425 430  
Glu Arg Ala Lys Arg Asn Gly Ser Ile Val Ser Met Asn Met Lys Asp  
435 440 445  
Ala Phe Ala Arg Ser Ile Glu Met Met Asp Ile Val Val Glu Lys Asn  
450 455 460  
Gly Glu Asn Met Gly Lys Lys Asp Lys Val Gln Asp Asn His Leu Ser  
465 470 475 480

Pro Asn Lys Trp Lys Trp Thr Lys Arg Thr Leu Ser Glu Thr Ser Ser  
                   485                  490                  495  
 Ser Lys Ser Phe Glu Thr Lys Glu Gln Gly Ser Pro Glu Lys Ala Arg  
                   500                  505                  510  
 Ser Ser Ser Pro Gln His Leu Asn Val Gln Gln Leu Glu Asp Met  
                   515                  520                  525  
 Tyr Asn Lys Met Ala Lys Thr Gln Ser Gln Pro Ile Leu Asn Thr Lys  
                   530                  535                  540  
 Glu Ser Ala Ala Gln Ser Lys Pro Lys Glu Glu Leu Glu Met Glu Ser  
                   545                  550                  555                  560  
 Ile Pro Ser Pro Val Ala Pro Leu Pro Thr Arg Thr Glu Gly Val Ile  
                   565                  570                  575  
 Asp Met Arg Ser Met Ser Ser Ile Asp Ser Phe Ile Ser Cys Ala Thr  
                   580                  585                  590  
 Asp Phe Pro Glu Ala Thr Arg Phe Ser His Ser Pro Leu Thr Ser Leu  
                   595                  600                  605  
 Pro Ser Lys Thr Gly Gly Ser Thr Ala Pro Glu Val Gly Trp Arg Gly  
                   610                  615                  620  
 Ala Leu Gly Ala Ser Gly Gly Arg Phe Val Glu Ala Asn Pro Ser Pro  
                   625                  630                  635                  640  
 Asp Ala Ser Gln His Ser Ser Phe Phe Ile Glu Ser Pro Lys Ser Ser  
                   645                  650                  655  
 Met Lys Thr Asn Asn Pro Leu Lys Leu Arg Ala Leu Lys Val Asn Phe  
                   660                  665                  670  
 Met Glu Gly Asp Pro Ser Pro Leu Leu Pro Val Leu Gly Met Tyr His  
                   675                  680                  685  
 Asp Pro Leu Arg Asn Arg Gly Ser Ala Ala Ala Val Ala Gly Leu  
                   690                  695                  700  
 Glu Cys Ala Thr Leu Leu Asp Lys Ala Val Leu Ser Pro Glu Ser Ser  
                   705                  710                  715                  720  
 Ile Tyr Thr Thr Ala Ser Ala Lys Thr Pro Pro Arg Ser Pro Glu Lys  
                   725                  730                  735  
 His Thr Ala Ile Ala Phe Asn Phe Glu Ala Gly Val His Gln Tyr Ile  
                   740                  745                  750  
 Asp Ala Asp Thr Asp Asp Glu Gly Gln Leu Leu Tyr Ser Val Asp Ser  
                   755                  760                  765  
 Ser Pro Pro Lys Ser Leu Pro Gly Ser Thr Ser Pro Lys Phe Ser Thr  
                   770                  775                  780  
 Gly Thr Arg Ser Glu Lys Asn His Phe Glu Ser Ser Pro Leu Pro Thr  
                   785                  790                  795                  800  
 Ser Pro Lys Phe Leu Arg Gln Asn Cys Ile Tyr Ser Thr Glu Ala Leu  
                   805                  810                  815  
 Thr Gly Lys Gly Pro Ser Gly Gln Glu Lys Cys Lys Leu Glu Asn His  
                   820                  825                  830  
 Ile Ser Pro Asp Val Arg Val Leu Pro Gly Gly Ala His Gly Ser  
                   835                  840                  845  
 Thr Arg Asp Gln Ser Ile  
                   850

<210> 13  
 <211> 806  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human voltage-gated potassium channel Kv2.2

<400> 13  
 Met Ala Glu Lys Ala Pro Pro Gly Leu Asn Arg Lys Thr Ser Arg Ser  
     1                  5                  10                  15

Thr Leu Ser Leu Pro Pro Glu Pro Val Asp Ile Ile Arg Ser Lys Thr  
     20                       25                       30  
 Cys Ser Arg Arg Val Lys Ile Asn Val Gly Gly Leu Asn His Glu Val  
     35                       40                       45  
 Leu Trp Arg Thr Leu Asp Arg Leu Pro Arg Thr Arg Leu Gly Lys Leu  
     50                       55                       60  
 Arg Asp Cys Asn Thr His Glu Ser Leu Leu Glu Val Cys Asp Asp Tyr  
     65                       70                       75                       80  
 Asn Leu Asn Glu Asn Glu Tyr Phe Phe Asp Arg His Pro Gly Ala Phe  
     85                       90                       95  
 Thr Ser Ile Leu Asn Phe Tyr Arg Thr Gly Lys Leu His Met Met Glu  
     100                       105                       110  
 Glu Met Cys Ala Leu Ser Phe Gly Gln Glu Leu Asp Tyr Trp Gly Ile  
     115                       120                       125  
 Asp Glu Ile Tyr Leu Glu Ser Cys Cys Gln Ala Arg Tyr His Gln Lys  
     130                       135                       140  
 Lys Glu Gln Met Asn Glu Glu Leu Arg Arg Glu Ala Glu Thr Met Arg  
     145                       150                       155                       160  
 Asp Gly Glu Gly Glu Glu Phe Asp Asn Thr Cys Cys Pro Asp Lys Arg  
     165                       170                       175  
 Lys Lys Leu Trp Asp Leu Leu Glu Lys Pro Asn Ser Ser Val Ala Ala  
     180                       185                       190  
 Lys Ile Leu Ala Ile Val Ser Ile Leu Phe Ile Val Leu Ser Thr Ile  
     195                       200                       205  
 Ala Leu Ser Leu Asn Thr Leu Pro Glu Leu Gln Glu Thr Asp Glu Phe  
     210                       215                       220  
 Gly Gln Leu Asn Asp Asn Arg Gln Leu Ala His Val Glu Ala Val Cys  
     225                       230                       235                       240  
 Ile Ala Trp Phe Thr Met Glu Tyr Leu Leu Arg Phe Leu Ser Ser Pro  
     245                       250                       255  
 Asn Lys Trp Lys Phe Phe Lys Gly Pro Leu Asn Val Ile Asp Leu Leu  
     260                       265                       270  
 Ala Ile Leu Pro Tyr Tyr Val Thr Ile Phe Leu Thr Glu Ser Asn Lys  
     275                       280                       285  
 Ser Val Leu Gln Phe Gln Asn Val Arg Arg Val Val Gln Ile Phe Arg  
     290                       295                       300  
 Ile Met Arg Ile Leu Arg Ile Leu Lys Leu Ala Arg His Ser Thr Gly  
     305                       310                       315                       320  
 Leu Gln Ser Leu Gly Phe Thr Leu Arg Arg Ser Tyr Asn Glu Leu Gly  
     325                       330                       335  
 Leu Leu Ile Leu Phe Leu Ala Met Gly Ile Met Ile Phe Ser Ser Leu  
     340                       345                       350  
 Val Phe Phe Ala Glu Lys Asp Glu Asp Ala Thr Lys Phe Thr Ser Ile  
     355                       360                       365  
 Pro Ala Ser Phe Trp Trp Ala Thr Ile Thr Met Thr Thr Val Gly Tyr  
     370                       375                       380  
 Gly Asp Ile Tyr Pro Lys Thr Leu Leu Gly Lys Ile Val Gly Gly Leu  
     385                       390                       395                       400  
 Cys Cys Ile Ala Gly Val Leu Val Ile Ala Leu Pro Ile Pro Ile Ile  
     405                       410                       415  
 Val Asn Asn Phe Ser Glu Phe Tyr Lys Glu Gln Lys Arg Gln Glu Lys  
     420                       425                       430  
 Ala Ile Lys Arg Arg Glu Ala Leu Glu Arg Ala Lys Arg Asn Gly Ser  
     435                       440                       445  
 Ile Val Ser Met Asn Leu Lys Asp Ala Phe Ala Arg Ser Met Glu Leu  
     450                       455                       460  
 Ile Asp Val Ala Val Glu Lys Ala Gly Glu Ser Ala Asn Thr Lys Asp  
     465                       470                       475                       480  
 Ser Ala Asp Asp Asn His Leu Ser Pro Ser Arg Trp Lys Trp Ala Arg  
     485                       490                       495

Lys Ala Leu Ser Glu Thr Ser Ser Asn Lys Ser Phe Glu Asn Lys Tyr  
 500 505 510  
 Gln Glu Val Ser Gln Lys Asp Ser His Glu Gln Leu Asn Asn Thr Phe  
 515 520 525  
 Ser Ser Ser Pro Gln His Leu Ser Ala Gln Lys Leu Glu Met Leu Tyr  
 530 535 540  
 Asn Glu Ile Thr Lys Thr Gln Pro His Ser His Pro Asn Pro Asp Cys  
 545 550 555 560  
 Gln Glu Lys Pro Glu Arg Pro Ser Ala Tyr Glu Glu Glu Ile Glu Met  
 565 570 575  
 Glu Glu Val Val Cys Pro Gln Glu Gln Leu Ala Val Ala Gln Thr Glu  
 580 585 590  
 Val Ile Val Asp Met Lys Ser Thr Ser Ser Ile Asp Ser Phe Thr Ser  
 595 600 605  
 Cys Ala Thr Asp Phe Thr Glu Thr Glu Arg Ser Pro Leu Pro Pro Pro  
 610 615 620  
 Ser Ala Ser His Leu Gln Met Lys Phe Pro Thr Asp Leu Pro Gly Thr  
 625 630 635 640  
 Glu Glu His Gln Arg Ala Arg Gly Pro Pro Phe Leu Thr Leu Ser Arg  
 645 650 655  
 Glu Lys Gly Pro Ala Ala Arg Asp Gly Thr Leu Glu Tyr Ala Pro Val  
 660 665 670  
 Asp Ile Thr Val Asn Leu Asp Ala Ser Gly Ser Gln Cys Gly Leu His  
 675 680 685  
 Ser Pro Leu Gln Ser Asp Asn Ala Thr Asp Ser Pro Lys Ser Ser Leu  
 690 695 700  
 Lys Gly Ser Asn Pro Leu Lys Ser Arg Ser Leu Lys Val Asn Phe Lys  
 705 710 715 720  
 Glu Asn Arg Gly Ser Ala Pro Gln Thr Pro Pro Ser Thr Ala Arg Pro  
 725 730 735  
 Leu Pro Val Thr Thr Ala Asp Phe Ser Leu Thr Thr Pro Gln His Ile  
 740 745 750  
 Ser Thr Ile Leu Leu Glu Glu Thr Pro Ser Gln Gly Asp Arg Pro Cys  
 755 760 765  
 Trp Ala Leu Arg Phe Gln Arg Leu Val Arg Asp Leu Pro Lys Gly Cys  
 770 775 780  
 Pro Pro Gly Phe Pro Ser Arg Asn Cys Ser Leu Ser Leu Gln Glu Arg  
 785 790 795 800  
 Gly Gly Ala Ser Leu Lys  
 805

<210> 14  
 <211> 26  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> DOMAIN  
 <222> (1)..(26)  
 <223> S6 domain of voltage-gated potassium channel  
 Kv10.1

<400> 14  
 Phe Phe Ala Phe Leu Cys Ile Ala Phe Gly Ile Ile Leu Asn Gly Met  
 1 5 10 15  
 Pro Ile Ser Ile Leu Tyr Asn Lys Phe Ser  
 20 25

<210> 15  
<211> 26  
<212> PRT  
<213> Homo sapiens

<220>  
<221> DOMAIN  
<222> (1)..(26)  
<223> S6 domain of voltage-gated potassium channel Kv6.1

<400> 15  
Val Val Ala Leu Ser Ser Ile Leu Ser Gly Ile Leu Leu Met Ala Phe  
1 5 10 15

Pro Val Thr Ser Ile Phe His Thr Phe Ser  
20 25

<210> 16  
<211> 26  
<212> PRT  
<213> Homo sapiens

<220>  
<221> DOMAIN  
<222> (1)..(26)  
<223> S6 domain of voltage-gated potassium channel Kv2.1

<400> 16  
Ile Val Gly Gly Leu Cys Cys Ile Ala Gly Val Leu Val Ile Ala Leu  
1 5 10 15

Pro Ile Pro Ile Ile Val Asn Asn Phe Ser  
20 25

<210> 17  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Kv10.1-specific amplification primer

<400> 17  
tgggctgcct gctgtcttc at 22

<210> 18  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Kv10.1-specific amplification primer

<400> 18  
ctctccccctc tccctgcgtta tggt 24